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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

US-09-455-486-6 2351 1 MESISMMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

88757 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O58896 methanococc		macaca	P79763 gallus gall	3 sacchar	Q12333 saccharomyc	P23945 homo saplen	P49059 sus scrofa	P31122 escherichta		ď	079421 branchiosto	Q15743 homo sapien		y genome	ğ								O15770 plasmodium		P33390 desulfovibr	P03910 bos taurus	Q10934 caenorhabdi	P46896 gallus gall		S	31 c	Ŋ
SUMMARIES	A	F4RE METUA	F4RE_METTH	FSHR_MACEA	FSHR_CHICK	FRE6 YEAST	FRE7_YEAST	FSHR_HUMAN	FSHR_PIG	YDEA ECOLI	NPT1_MOUSE	RF3_SACBA	NU4M_BRALA	GP68_HUMAN	POLG_YEFV1	POLG_YEFV2	FSHR_BOVIN	FSHR_RAT	FRE1_YEAST	PHSC_ECOLI	NUCC_ARATH	SECY_CYAPA	FSHR_SHEEP	NU4M_BRAFL	GSHR_PLAF7	VL1_REOVD	HMC3_DESVH	NU4M_BOVIN	YT25_CAEEL	GTR1_CHICK	YHL6_YEAST	YJK9_YEAST	FAS1_CANAL	TPS1_YEAST
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	Query Match Length		232	695	693	712	629	695	695	386	465	476	452	365	3411	3411	695	692	989	261	393	492	695	452	499	1233	388	459	521	490	883	1769	2037	495
dР	Query Match	5.	5.1	4.7	4.6	4.6	4.6	4.6	4.4	4.4	4.4	4.3	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4 · I	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	6°€	•	3.9	٠.	9.6
	Score	13	120.5	111.5	109	109	107.5	107.5	104.5	104	103	100	99.5	66	96	9	97.5	9	96.5	96	95	94.5	94.5	93.5		. 93.5	69	63	93			92.5	92.5	91.5
	Result No.	-	7	3	4	S	9	7	a o	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	. 06	31	32	. 33

P25870 dictyostell	v,		Q62795 rattus norv			034931 baclilus su		079671 pelomedusa	_	Ψ,	Ψ	
CLH_DICDI	SSU1_YEAST	YPNP_BACSU	NPT1_RAT	KR11_YEAST	HXTC_YEAST	YTMM_BACSU	NU2M_XENLA	NU2M_PELSU	NUCC_ORYSA	YBL4_YEAST	FSHR_EQUAS	
Т	-	-	-	Н	П	-	7	⊣	H	~	П	
1694	458	445	465	260	564	235	345	346	393	433	687	
3.9	9.6	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.09	3.8	
91.5	91	90.5	90.5	90.5	90.5	06	89.5	89.5	89.5	89.5	89.5	
34	35	36	. 37	38	39	40	41	42	43	44	45	
				-								

ALIGNMENTS

RESULT I FARE_METJA STANDARD; PRT; 223 AA. AC 058896:			RN 118 SEQUENCE FROM N.A. RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067; RX MEDLINE-96337999; PubMed-8688087; RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,	RA SULCON G.G., blacke J.A., Flr2gefald L.M., ClayLON K.A., GOCSAyne J.D., RA Kerlavage A.R., Dougherty B.A., Tomb JF., Adams M.D., Reich C.I., RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., RA Scott J.L., Geoglagen N.S.M., Weldiman J.F., Fuhrmann J.L., Nguyen D., Pa Hitterhack T. D. Weller J. M. Weldimann J.E., Fuhrmann J.L., Nguyen D.,		Screen	CC -1- SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entitles regulares a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@lsb-sib.ch).	
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34; Gaps Query Match 5.7%; Score 133; DB 1; Length 223; Best Local Similarity 21.9%; Pred. No. 0.0063; Matches 46; Conservative 52; Mismatches 78; Indels

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37 GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV------THHEDALT 84

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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Andredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Adredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wlerzbowski J., Glbson R., Juwan I. N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shlmer G., Goyal A., Pietrovski S., Church G.M., Danlels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Complete genome sequence of Methanobacterlum thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7155-7155(1997).

-I. FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADP(+) AND THE REDUCTION OF NADP(+) WITH F420H(2). PROBABLY COUPLES THE NADP-DEPENDENT OXIDATION OF CO(2) TO METHANE (ANABOLIC FUNCTION) (BY
                                                                                                       -- SNNMRINOYPE-SNAEYL 133
                                                               EGDVVILSLPYEYTLSTIKQLKEELKGKIVVSIGVPLATAIGDKPTRLLFPPDGSVAEMV 126
                                                                                        134 ASLEPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFI-PIDL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NNMRINOYPESN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
         GTGDQGFGLALRLAK-NNKIIIGSRKKEKAEEAAKKAKEILKQRGIEADIIGLENKDAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 KVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: NADPH + COENZYME F420 = NADP(+) + REDUCED
                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlcE60ABC8474296 CRC64;
                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 120.5; DB 1; 23.8%; Pred. No. 0.052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 -DALTKINIIFVAIH-REHYTSLWDLRHLLVGKILIDVS---
                                     KTNIIFVAIHREH-YTSLWDLRHLLVGKILIDV-----
                                                                                                                                                                                                                                         232 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 GSLSSAREIENLPLRLFTLWRGPVVVAISL 222
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DELTA H:
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                (Rel. 37, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                 Methanobacterium
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SEQUENCE 23
                                                                                                                                                                                                                                                                   15-DEC-1998
                                                                                                                                                                                                                                           F4RE_METTH
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                                                               130 AEYLASLF---PDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186
67 PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADENYLATE CYCLASE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONG: TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH_CHH_TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOLLICLE STIMULATING HORMONE RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1143; FSHRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Phosphoryiation; Repeat; Leucine-repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.;
"Molecular closing of the testicular follicle stimulating horm
receptor of the non human prince Macaca fascicularis and
identification of multiple transcripts in the testis.";
Blochem. Blochys. Res. Commun. 196:1065-1072(1993).
-1- FUNCTION: RECEPTOR FOLLICLE STIMULATING HORMONE. THE A
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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PRINTS; PR01143; FSHRECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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PFAM, PF00560; LRR, 4.
PFAM, PF01462; LRRNT; 1.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPR002131, -.
INTERPRO; IPR002272; -.
PFAM; PF00001; 7tm_1; 1.
PFAM; PF00560; LRR; 2.
                                                                                                                                    Gene 197:121-127(1997).
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191
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    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                               122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
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                                                                                                                                                                                                                                                                                                                                                                   HEDALTKINIIFVAIHREHYTSLWDLRHLLVG---------KILLDVSNNMR 121
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P79763; Q90719;
01-N0V-1997 (Rel. 35, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40. Last annotation update)
POLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 RSTYNLKKLP----SLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQEV
                                                                                                                                    EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                     183;
                                                                                                                                                                                                                                                                                                         Length 695;
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 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                          EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
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                              3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                         CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                      4.7%; Score 111.5; DB 1;
17.0%; Pred. No. 0.83;
tive 75; Mismatches 151;
                                                                                                                                                                                                                                             SIMILARITY
                                                             (POTENTIAL)
                                                                                                                        (POTENTIAL)
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293
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nes 84; Conserv
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DOMAIN
TRANSMEM
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DISULFID
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TD FSHR_CHICK
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DT 01-NOV
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN:
MEDLINE-97057887; Dubmed-8902217;
You S., Bridgham J.T., Foster D.N., Johnson A.L.;
Characterization of the chicken follicle-stimulating hormone
receptor (cr8H-R) complementary deoxyribonucleic acid, and expression
of cFSH-R messenger ribonucleic acid in the ovary.";
Biol. Reprod. 55:1055-1062(1996).
--- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                Wakabayashi N., Suzuki A., Hoshino H., MIshimori K., Mizuno S.; "The cDNA cloning and transient expression of a chicken gene encoding a follicle-stimulating hormone receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
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PRINTS, PR00373; GLYCHORMONER.
PRINTS, PR00137; GLYCHORMONER.
PRINTS, PR001143; FSHRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE; PS002262; G_PROTEIN_RECEP_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Phosphorylation; Repeat; Leucine_repeat.
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2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (PO
N-LINKED (GLCNAC. . . ) (PO
N-LINKED (GLCNAC. . . ) (PO
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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MEDLINE-97473503; PubMed-9332357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 KODLGEQTGKRKHRRSAAEDYISHYGTRFGPVENEFDYGLCNEVVDFVCSPKPDAFNPCE 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 IENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE------FSFIQ 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ENKNGIQE 184
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                        ---PKL----- 97
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etaceae; Saccharomyces.
        .) (POTENTIAL)
                                                                                                                                                                                                                                          72; Mismatches 173; Indels 238;
                                                                                                                                                                                                    Length 693;
                        G -> D (1N REF. 2).

C -> A (1N REF. 2).

K -> R (1N REF. 2).

I -> T (1N REF. 2).

Y -> L (1N REF. 2).

46F98699635AlbEC CRC64;
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15-DEC-1998 (Rel. 37, Last annotation update)
FERRIC REDUCTASE TRANSWEMBRANE COMPONENT 6 PRECURSOR
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17.2%; Pred. No. 1
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      N-LIHKED
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Submitted (JAN-1995) to the F
-!- COFACTOR: FAD (PROBABLE).
                                                                                                                                                                                                                      Best Local Similarity 17.2
Matches 100: Conservative
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693 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 DRS-GILAFTOFPLIIIFTARNSFLEFLTGVKFNSF-----ISFHKWIGRIMVLNATI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 FPDSLIVKGFNVVSAMALQLGPKDASRQVY1CSNNIQARQQVIELARQLNFIPIDLGSLS 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AVTSIPSVSNALNWREFSFIQSTLGYVALLI---STFHVLIY-GWKRAFE----EE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 IIAVFFHMSHYNGLNRALFASRFVNYIRGHFVLPTFLVD----KHANHFKFLNVEVFTGL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 SAREIENLPLRLFTLWRGPVVVAISLATFFFL-YSFVRDVIHPYARNQQSDFYKIPIEIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 NKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMV
SUBCELLULAR LOCATION: INTEGRAL MFMBRANE PROTEIN (POTENTIAL)
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PRAM; PF01794; Ferric_reduct; 1.
Blectron transport; Transmembrane; Iron transport; FAD; HAD;
Glycoprotein; Ignal; Multigene family.
SIGNAL 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 712;
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51; Mismatches 119;
                        CYBB FAMILY
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Best Local Similarity 18.8%; Pred. No. 1.
Matches 72; Conservative 51; Mismatche
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                        -! - SIMILARITY: BELONGS TO THE FRE /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:::| |:::| |:::| |CQARHA----QRWKASDWWR-----SGVPPILFLNLLWLSSLPIARRH 262
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                                                                                                                                                                                                                                                       arm of yeast
                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                     Casanayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,
Lafuente M.J., Gancedo C., Arino J.;
"DNA sequence analysis of a 13 kbp fragment of the left arm of ye
chromosome XV containing seven new open reading frames.";
Yeast 11:1281-1288(1955).
-i - COFACTOR: PAD (PROBNALE).
-i - SUBCELLULAR LOCATION: INFEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i - SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL,
N-LINKED (GLCNAC, , ,) (POTENTIAL)
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2384480E9289C16F CRC64;
                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FERRIC REDUCIASE TRANSMEMBRANE COMPONENT 7 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
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Pred. No. 1.4;
                          629 AA.
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                           PRT;
                                                                                                                                                       Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                            STRAIN=S288C / FY1679;
MEDLINE-96132030; PubMed-8553699;
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PFAM; PF01794: Ferr1c_reduct; 1.
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INTERPRO, IPR002916; -.
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                          STANDARD;
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66
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629 AA;
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                                                                                                                                                                                SEQUENCE FROM N. A
                                                                                                             FRE7 OR YOL152W.
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SIGNAL
                         FRE7_YEAST
012333;
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Best Local S.
Matches 57
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SEQUENCE
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RESULT 6
FRE7_YEAST
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MEDLINE-96363672; PubMed-8747461;
Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,
Hendrickson W.A., el Tayar N.;
"Structural predictions for the llgand-binding region of glycoprotein
hormone receptors and the nature of hormone-receptor interactions.";
Structure 3:1341-1353(1995).
-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
 --LIYGWKRAFEEEYYR- 425
                                   263 FYEIFLQLHW----ILAVGFYISLF---YHVYPELNSHMYLVATIVVW---FAQLFYRL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kelton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,
Rosenthal J.L., Overton S.A., Wands G.D., Kuzeja J.B., Luchette C.A.,
                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A SHORT FORM OF THE TESTICULAR PROTEIN IS
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cioning of the human follicle stimulating hormone receptor and expression in COS-7, CHO, and Y-1 cells."; Cell. Endocrinol. 89:141-151(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gromoil J., Dankbar B., Gudermann T.;
Characterization of the 5' flanking region of the human follicle-
stimulating hormone receptor gene.":
Mol. Cell. Endocrinoi. 102:93-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minegish T., Nakamura K., Takakura Y., Ibuki Y., Igarashi "Cloning and sequencing of human FSH receptor cDNA.";
Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tilly L.T., Alhara T., Nishimori K., Jai X.-C., Billig B
Kowalski K.I., Perias E.A., Hsueh A.J.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulating hormone receptor.";
Blochem. Biophys. Res. Commun. 188:1077-1083(1992)
                                                                                                                                                                                                          695 AA.
--SVSNALNWREFSFIQSTLGYVALLISTFHV--
                                                                                                                                                                                                          PRT;
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MEDLINE-95011044; PubMed-7926278;
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                                                                         ----FYTPPNFVLALVLPSIVIL 444
                                                                                                   312 AVKGYLRPGRSFMASTIANVSIV 334
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                                                                                                                                                                                                                                                21, Created),
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                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                              01-MAR-1992
                                                                                                                                                                                                          FSHR_HUMAN
                                                                                                                                                                                                                                                                                                                          RECEPTOR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATACELLAN (FOILMING)
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-SING (IN SHORT TESTICULAR ISOPORM).
MISSING (IN SHORT TESTICULAR ISOPORM).
S -> R (IN REF. 4).
N -> T (IN REF. 4).
  SHOWN HERE IS THAT OF THE LONG TESTICULAR PROTEIN.
TISSUE SPECIFICITY: SERYOLI CELLS AND OVARIAN GRANULOSA CELLS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0237; G_PROTEIN_RECEP_P1_1; 1.
PROSITE; PSSO462; G_PROTEIN_RECEP_F1_2: 1.
G_PLOCEAIn coupled receptor; Transmenbrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. FOLLICLE STIMULATING HORMONE EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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-> A (IN REF. 1).
-> S (IN REF. 1).
723B8E71F76D2CD5 CRC64;
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PRINTS; PR01143; FSHRECEPTOR.
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                                                                                                                                                                        EMBL, S59900, AAB26480.1; -. EMBL, M95489; AAA52478.1; -. EMBL, X68044; CAA48179.1; -. EMBL, S73199; AAB32071.1; -.
                                                                                                                                                              EMBL; M65085; AAA52477.1; -.
                                                                                                                                                                                                                                                                                                                  INTERPRO, IPRO0372; --
INTERPRO, IPRO01611; -
INTERPRO, IPRO02131; -
INTERPRO, IPRO02272; --
PFAM: PF0001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF01462; LRRNT; 1.
                                                                                                                                                                                                                       PIR, JN0122; JN0122.
PDB; JXUN; 15-18-97.
GCRDB; GCR_0071; --
GCRDB; GCR_0404; --
GCRDB; GCR_0588; --
GCRDB; GCR_0590: --
                                                                                                                                                                                                                                                                                                           INTERPRO; IPR000276; -.
                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00560; LRR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------LCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASEL 455
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P49059; 077514;
D1-FEB-1996 (Rel. 37, Last sequence update)
D1-OCT-2000 (Rel. 40, Last annotation update)
FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Porcine follicle-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/Genbank/DbBJ databases.
-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                             182 ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                           ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                                   247 RSTYNLKKLP-----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILROE 300
                                                                                                                                                                                                                                                                                                                                                                     ----KILIDVSNNMR 121
                                                                                                                                              122 INOYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASROVYICSNNIQARQOVIEL 181
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Sus.
Length 695;
                                                                                                                                                                       cloning, functional
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Pajot E., Grebert D., Salesse R.;
The porcine follitropin receptor: cDNA cloning, functional
expression and chromosomal localization of the gene.";
Gene 163:257-261(1995).
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Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.,
la Barbera A.R.;
                                      Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae;
 DB 1;
                 ; Pred. No. 1.6; 77; Mismatches 148;
                                                                        79 HEDALTKINIIFVAIHREHYTSLWDLRHLLVG------
                                                                                                                                                                                                                                                                                               242 NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY-----
4.6%; Score 107.5; 17.0%; Pred. No. 1.6
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MEDLINE-96011644; PubMed-7590277;
                                      Conservative
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516 ICLPMDIDSPLSQL 529
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               Best Local Similarity
Matches 84; Conserv
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               FOLLICLE STIMULATING HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL).

(POTENTIAL).

CYTOPLASMIC (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                          PERM: PP00001. Thm. 1.1 1.

PEAM: PP00560: LRR: 4.

PENM: PP01462. LRRWT: 1.

PRINTS: PR00373: GLYCORNONER.

PROSITE: PS00237: G_PROTEIN_RECEP_FI_I; 1.

PROSITE: PS00237: G_PROTEIN_RECEP_FI_I; 1.

PROSITE: PS00263. G_PROTEIN_RECEP_FI_2; 1.

G-protein coupled receptor: Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine_repeat.
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N-LINKED (GLCNAC, .) (POTENTIAL).
N-LINKED (GLCNAC, .) (POTENTIAL).
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EMBL; AF025377; AAC24981.1; -
HSSP; P23945; 1XUN.
                                                                                                                                                    3CRDB, GCK_____,
INTERPRO, IPR000276; -.
                                                                                                                                                                                          INTERPRO; IPR002131; -.
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MEDLINE-97251357; PubMed-9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
                                                                                                                                                                                      77 THHEDALTKTNIIFVAIHREHYTSLWDLRHLLVG---------KILIDVSNN I19
                                                                                                                                                                                                                                                                                    120 MRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PIVAITLL----- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YSLCLPMRRSERYLFLNMAYQQVHANIENSWNE 351
                                                                                             LPNG-INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=KIZ '/ MG165A;
STRAIN=KIZ '/ MG165A;
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                       61 IPKGAFSGFGDLEKI-----EISQNDVLEVIEAN----VFSNLPKL-----
                                                                                                                                                                                                                                                                                                                                                                                  · 180 ELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPY
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Escherichia.
                                                 199;
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Length 695;
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                                                 Indels
; Score IO4.5; DB 1;
; Pred. No. 2.6;
91; Mismatches 169;
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                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, INNER MEMBRANE
  Kasal H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito I Sampel G., Seki Y., Sivasundariam S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T., Corresponding to the Bscherichia coli K-12 genome corresponding to the 28 0-40.1 min region on the ilnkage map.";
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SIMILARITY: TO S.LIVIDANS CHLORAMPHENICOL RESISTANCE PROTEIN
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                                                                                                                                                                                                     SEQUENCE OF 217-396 FROM N.A.
MEDLINE-93186717; Pubmed-8383113;
Cohen S.P., Hacchler H., Levy S.B.;
Cohetic and functional analysis of the multiple antibiotic resistance (mar) locus in Escherichia coli.";
J. Bacteriol. 175:1484-1492(1993).
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ECOGENE; EG11636; YDEA.
INTERPRO; IPR001066; -.
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15-JUL-1998 (Rel. 36, Last sequence update)
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN i (SODIUM/PHOSPHATE COTRANSPORTER 1) (NA(+)/PI COTRANSPORTER 1) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 1) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 1).
SLC17A1 OR NP11.
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Am. J. Physioi. 268:F1036:F1045(1995).
-!- FUNCTION: IMPORTANT FOR THE RESORPTION OF PHOSPHATE BY THE KIDNEY.
NAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
240 ARN---QQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLE 296
                                                                                                                                                                                                                                     ----ALNWREFSF1OST 397
                                                                                                                                                                                                                                                                                         310 IAMMIIGLGMQVKVLALAPDATDVAMALFSGIFNIGIGAGALVGNQVSLHWS-----MSM 364
                                                                                                                 297 TWLOCRKOLGILSFFFAMVHVAYSLCLPMRRSERYLFLNMAYOQVHANIENSWNEEEVWR
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                                                       ----ATALLLLGGAGIIGSVIFGKLGNQYAS----
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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C67EE25A2C291EEF CRC64;
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MEDLINE-95335846; PubMed-7611445;
Chong S.S., Kozak C.A., Liu L., Kristjansson K., Dunn S.T.,
Bourdeau J.E., Hughes M.R.;
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465 A
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Q61983;
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                                                                                                                                                                                                                                                                                                                                                                                             254 NPYFVNAFSINI------FTNLAKEKIFTNIYNKLYSDYKINQINNHIPYYNYLK 302
                                                                                                                                                                                                                                                                                                                                                      162 SRQVYICSNNIQARQOVIELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAIS 221
                                                                                                                                                                                                           104 LRHLLVGKILIDVSNNMRINQYPESNAEYLASLF--PDSLIVKGFNVVSAWALQLGPKDA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 LATFFILYSFVRDV1HPYARNQOSDFYKIP----IEIVNKTLPIVAITLLSLVYLAGLLA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa: Chordata; Cephalochordata; Branchlostomidae;
Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spruyt N., Delarbre C., Gachelin G., Laudet V.;
"Complete sequence of the amphloxus (Branchiostoma lanceolatum)
mitochondrial genome: relations to vertebrates.";
Nucleic Acids Res. 26:3279-3285(1998).
-i- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                          NPKFASEFFPHVVDVTHHEDALTKTNI ----IFVAIHREHYT------
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branchiostoma lanceolatum (Common lancelet) (Amphioxus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
                                                                                                                                                                                                                                                      303 INNKLPIKNIMDIKNNYWLAGFTAADGSFLSSMYNPKDFLLFKDM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 99.5; DB 1;
20.1%; Pred. No. 3.7;
tive 56; Mismatches 139;
          85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 AA
          48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98292550; PubMed-9628930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00361; oxidored_q1: 1.
PFAM; PF001059; oxidored_q5_N; 1.
Oxidoreductase; NaD; Ubiquinone; SEQUENCE 452 AA: 49940 MW; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y16474; CAA76256.1; -. INTERPRO; IPR000260; -. INTERPRO; IPR001750; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 4.2%
Best Local Similarity 20.1%
Matches 95, Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ND4 OR NAD4 OR NADH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 AAYQLYYGTKY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 DNYDYYYYNKY 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NU4M_BRALA
079421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NU4M_BRALA
                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
          Matches
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                                                                . 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFICDLIGWPMVFYIFGIVGCVLSLSWFFLFFDDPKD--HPYMSSSEKDYIISSLMQQAS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGRQSEDIKAMLKSLPLWAIILNSFAFIWSNSLLVTYTPTFISTVLHVNVRENGLLSSLP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 YLLAYICGILAGOMSDFFLTRK-----IFSIVTVRKLFTTLGSFCPVIFIMCLLYLSYN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 FYSTVIELTLA----NSTLSFSYCGOLINALDIAPRYYGELKAVTALIGMFGGLISSTLA 415
                                                                                                                                                                              :| : | : | : | : | : | 136 VCRVLQGIAQGTVSTGQHEIWVKWAPPLERGRITS-----MILSGFVM--GPFIVLLVS 187
                                                                                                                                                                                                                                                                                                                                                                                                                  --------AISLATFFFLYSFVRDVIHPYARNQOSDF------ 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LVYLAGILAAAYQLYYGTKYRFFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 RSERYLFLNMAYQQVHANIENSWNEEEVWRIEM---YISF--GIMSL----GLLSLLAV 376
                                                                                                                                           GKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPKDA---SRQVY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
Mitochondrion.
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                           ICSNNIQARQOVIELARQLNFI----PIDLGSLSSAREIENLPLRLFTLWRGPVVV----
4.4%; Score 103; DB 1: Length 465;
18.7%; Pred. No. 2.1;
Live 64; Mismatches 142; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YKIPIEIVNKTLPIVAITLLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: THE RF3 PROTEINS ARE RELATED TO THE MATURASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seraphin B., Simon M., Faye G.;
"The mitochondrial reading frame RF3 is a functional gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 TSIPSVSNALNWREFSFIQSTLGYVALLISTFHVL----IYGWKR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 AA; 57863 MW; ECB416C51DFFDA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 1;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MATURASE-LIKE RF3 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem. 262:10146-10153(1987),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00961; Intron_maturase; 1. Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-87280035; Pubmed-2440860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J03300: CAB23320.1; -.
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces uvarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001982
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Best Local Similarity
                                       Similarity
                 Local St. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RF3_SACBA
P05512;
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RF3_SACBA

J. Blol.

SEQUENCE

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25;
                                                                                                                                                                     109'VGKIL-----IDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDAS 162
                                                                                                                                                                                                                                                          163 ROVYICSNNIQAR-----QOVIELARQLNFIPIDLGSLSSAREIENLP-LRLFTLWRGPV 216
                                                                                                                                                                                                                                                                                                  80 OOHMVSESLIYQRVFVGCQVFLTGALVLAFMASDLLLFYIAFESTLLPTLMLTTRW-GAQ 138
                                                                                                                                 Gaps
                                                                                                                                                                                                  Indels 183;
                                                                                       Length 452;
e; Mitochondrion.
4067DB59EC184C7A CRC64;
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us-09-455-486-6.rsp

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RARATITITE
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                                        -----GSLPLL-ICLIGQYQMVGSL 173
                                                                      324
                                                                                                                                                                                                                 281 SLIAYSSVGHMALVVGGVLTGVAWGYNGAMVLMIAHGLVSSCLFCLANLWYERSSTRNLS 340
                                                                                                                                                                                                                                               403
                                                                                                                                                                                                                                                                 174 ALDLSYEGVFQLSYLVNF----W---WVGC----ILAFLVKLPLYGVHLWLPKAHVEA 220
                                                                                                                                                         221 PIAGSMVLAGVLLKLGGYGMMRVSLMWGATAMLSSEVFLALALWGIVVWGGICLRQTDLK 280
                                                                                                                                                                                                                                                                                                                                                                                                                 015743; 013334;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR68 (OVARIAN CANCER G PROTEIN-
COUPLED RECEPTOR 1) (OGR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: FOUND IN MANY TISSUES, INCLUDING SPLEEN, TESTIS, PERIPHERAL BLOOD LEUKOCYTES, BRAIN, LUNG, AND PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
            217 VVAISLATFFELYSFVRDVIHPYARNOQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLL
                                                                     A-----AAYQLYYGTKYRRFPPWLETWLOCRKQLGLLSFFFAMYHVAYSLCLP-----
                                                                                                                                                                                       ----HAN1E-----NSWNEEEVWR---
                                                                                                                                                                                                                                             --IEMYISFGIMSLG--LLSLLAVTSIPSVS------NALNWREFSFIQSTLGYVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapians (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu Y., Casey G.;
"Identification of human OGR1, a novel G protein-coupled receptor
that maps to chromosome 14.";
                                                                                                                                                                                                                                                                                                                       404 LISTFHVLIYG---WKRAFEEEYYRFY--TPPNFVLAL--VLPSIV1LDLLQL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An S., Goetzl E.J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN RECEPTOR.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                               ---MRRSERYLFLNM-
                                                                                                                                                                                                                                                                                                                                                                                                          365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-OVARIAN CARCINOMA;
MEDLINE-96299795; PubMed-8661159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOT DETECTABLE IN OVARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U48405; AAC50596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 35:397-402(1996).
                                        139 KERYQAGIYEMPETLV---
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPRO00276; PFAM; PF00001: 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCRDB; GCR_1937; -. GCRDB: GCR_1960; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                     ---AYOOV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPR68 OR OGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601404;
                                                                                                                                                                                                                                                                                                                                                                                                        GP68_HUMAN
                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
GP68_HUMAN
                                                                                                                              325
                                                                                                                                                                                     337
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POLG_YEFV1 STANDARD; PRT; 3411 AA.

p03314; 042028;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (COMTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX DEROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN EN NOSTRICTURAL
PROTEINS NS1, NS2A, NS2B, NS3B, NA3A AND NS4B; HELICASE (NS3); RNA-DIRECTED
Yellow fever virus (strain 17D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 VNKTL-PIVAITLLSLVYLAGLLAAAYOLYYGTKYRRPPPWLETWLOCRKOLGLLSPFFA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 VADLFYICSLPFW------LQYVLQHDNWSHGDLSCQVCGILLYENIYI-SVGFLGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 IHQTLAPVVYVTVL----VVGFPANCLSLYFG------YLQ--IKARNELGVYLCNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 MYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      **Intansa J.H.; ; ... sequence of yellow fever virus: implications for flavivirus gene expression and evolution."; Science 229:726-733(1985).

-1. FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOSIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
G_PROTEIN_RECEP_FI_1; 1.
G_PROTEIN_RECEP_FI_2; 1.
receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                               G -> R (IN REF. 2).
S -> T (IN REF. 2).
05919AFD5B842CCD CRC64;
                                                                          1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                    EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       refrow tever virus (strain 1/D).
Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2%; Score 99;
22.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 HYPLQAWQRAI--NYYRFLVGFLFPICLLLAS
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MEDLINE-85272570; Pubmed-4023707;
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263
284
365
172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA;
                                      3-protein coupled
 PROSITE: PS00237:
PROSITE; PS50262;
                                                                                                                                                                                         137
159
206
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CONFLICT
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Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEDCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C.
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NONSTRUCTURAL PROTEIN NSI.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
HELLCASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4A.
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ATP (POTENTIAL).
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PFAM: PF00048: FIBVI_M: 1.
PFAM: PF00048: FIBVI_MS1: 1.
PFAM: PF01002: FIBVI_MS2B: 1.
PFAM: PF01350: FIBVI_MS2B: 1.
PFAM: PF01350: FIBVI_MS2B: 1.
PFAM: PF001349: FIBVI_MS5: 1.
PFAM: PF01003: FIBVI_MS5: 1.
PFAM: PF000069: FIBVI_MS5: 1.
PFAM: PF000049: FIBVI_MS5: 1.
PFAM: PF00107: FIBVI_MS5: 1.
PFAM: PF00107: FIBVI_MS1: 1.
PFAM: PF01570: FIBVI_MS1: 1.
PFAM: PF01570: FIBVI_MS1: 1.
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INTERPRO; IPR000752; -.
INTERPRO; IPR001122; -.
INTERPRO; IPR001157; -.
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                                                                 PROTEIN C AND MRNA
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INTERPRO; IPR002535; -
                                                                                                                                                                                                                                                                                                                                                                        NTERPRO; 1PR000069;
                                                                                                                                                                                                                                                                                                                                                                                                                   NTERPRO: IPR000336;
                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO00208
                                                                                                                                                                                                                                                                                                                                lsva.
                                                                                                                                                                                                                                                                                              PIR; A03914; GNWVY
HSSP; P14336: 1cm
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NP_BIND
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PLMALLTPVTWAEVRLAAAMFFCAVVIIGVLHONFKDTS-------MQKTIPLVALTL 1329
                                                                                                                                                                                                                                                                                                                        1229 RERLVLTLG----AAMVETALGGVMG-----GLWKYLNAVSLCILTINAVASRKASNTIL 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAFQEMENFLGPIAVGGLLMMLVSVAGRVDGLELKRLGEVSWEEEAEISGSSARYDVALS 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (ReI. 17, Created)
01-FEB-1991 (ReI. 17, Last sequence update)
15-DEC-1994 (ReI. 37, Last sequence update)
61-OFEB-1994 (ReI. 37, Last annotation update)
6ENOME POLYPROTEIN (CONTAINS: CAPSID FROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NB1, NS2A, NS2A, ANS AND NS4B; HELICASE (NS3); RNA-DIRECTED
FRUA POLYMERASE (EC 2, 7.7,48) (NS5)].
FRUA FOLYMERASE (EC 2, 7.7,48) (NS5)].
                                                                                                                                                                                                                                      107 LLVGKI-LID-----VSNNMRINQYPE-SNAEYLA-----SLFPDSLIVKGFNVVSAWA- 153
                                                                                                                                                                                                                                                                                            ----LOLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLS--SAREIENLPL 206
                                                                                                                                                                                                                                                                                                                                                                              RLFTLWRGPVVVA1SLATFFFLYSFVRDVIHPYARNQOSDFYKIPIEIVNKTLPIVAITL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLVYLA----GLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPMRRSERYL-----FLNMAYQQVHANI------ENSWNEE-EVWRIEMYISFGIM 366
                                                                                                                                                                     Gaps
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SEQUENCE FROM N.A.
MEDLINE-89282413: PubMed-2734112;
Dupuy.A., Despres P., Cahour A., Girard M., Bouloy M.;
"Nucleotide sequence comparison of the genome of two 17D-204 yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fever vaccines...

Nucleic Acids Res. 17:3989-3889(1989).

- FUNCTION: THE SMALL PROTEINS NS2A, NS2A AND NS4B ARE
HYDROPHOBIC. SUGGESTING A POSSIBLE MEMBRANG-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

- SUBUNIT: THE VIRION OF THIS VIRUS 1S A NUCLEOCARSID COVERED BY
LIPOPROTEIN BAND GLYCOPROTEIN E. THE BUNCLEDCARSID IS A COMPLEX OF
PROTEIN A AND GLYCOPROTEIN E. THE NUCLEOCABSID IS A COMPLEX OF
PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1330 TSYLCLTQPFLCLCAFLATRIFG---RRSIPVNEA-LAAAGLVGVLA------G
    (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                             4.2%; Score 98; DB 1; Length 3411; 22.2%; Pred. No. 49;
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N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
M, 680E0FACD23DCFA6 CRC64;
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                                                              379512
                                                                                                                                              Local Similarity 22.2% Local Similarity 22.2%
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2467
2320 233
2346 234
2467 246
3411 AA;
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P19901;
  CARBOHYD
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                                                                SEQUENCE
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POLG_YEFV2
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PFAM; PF00869; Flavi_glycoprot; 1.
PFAM: PF00949: Flavi_helicase; 1.
PFAM: PF00570; Flavi_propep; 1.
PGAM; PF01570; Flavi_propep; 1.
POLyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAJOR ENVELOPE PROTEIN E. NONSTRUCTURAL PROTEIN NS1. NONSTRUCTURAL PROTEIN NS28. NONSTRUCTURAL PROTEIN NS28.
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01349; Flavi_NS4B;
PF00972; Flavi_NS5; 1
                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO01850; -
                                                                                                                                                                                                                                                    INTERPRO; IPR001157; -
INTERPRO; IPR001528; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3411 AA;
                 PIR; S07757; GNWVYP
                                                                                                                                INTERPRO; IPRO00336
INTERPRO, IPRO00404
                                                                                                                                                                               INTERPRO; IPRO00487
INTERPRO; IPRO01122
INTERPRO; IPRO01122
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d d	1280	
δ	267	267 LSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLC 322
Dp	1330	1330 TSYLGLTQPFLGLCAFLATRIFGRRSIPVNEA-LAAAGLVGVLAG 1373
ć	323	323 LPWRRSERYLFLNMAYQQVHANIENSWNEE-EVWRIEMYISFCIM 366
g	1374	
oy	367	~
a	1434	1434 EQGEFKLLSEEKVPWDQVVWTSLALVGAALHPFALLLVLAGW 1475

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